

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/243,008A

Source: 1FW/6

Date Processed by STIC: 8/1/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 08/01/2005

PATENT APPLICATION: US/09/243,008A

TIME: 15:00:53

Input Set : A:\Seqlist.txt

Output Set: N:\CRF4\08012005\I243008A.raw

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4 <110> APPLICANT: Seed, Brian
5      Romeo, Charles
6      Kolanus, Waldemar
8 <120> TITLE OF INVENTION: Redirection of Cellular Immunity by
9      Receptor Chimeras
11 <130> FILE REFERENCE: 00786/270002
13 <140> CURRENT APPLICATION NUMBER: US 09/243,008A
14 <141> CURRENT FILING DATE: 1999-02-02
16 <150> PRIOR APPLICATION NUMBER: US 08/394,176
17 <151> PRIOR FILING DATE: 1995-02-24
19 <150> PRIOR APPLICATION NUMBER: US 08/203,866
20 <151> PRIOR FILING DATE: 1994-02-28
22 <150> PRIOR APPLICATION NUMBER: US 07/847,566
23 <151> PRIOR FILING DATE: 1992-03-06
25 <150> PRIOR APPLICATION NUMBER: US 07/665,961
26 <151> PRIOR FILING DATE: 1991-03-07
28 <160> NUMBER OF SEQ ID NOS: 41
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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33 <211> LENGTH: 1728
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <400> SEQUENCE: 1
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39 gcagccactc agggaaacaa agtggtgctg ggcaaaaaag gggatacagt ggaactgacc 120
40 tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180
41 attctgggaa atcagggtct cttcttaact aaagggtccat ccaagctgaa tgatcgcgct 240
42 gactcaagaa gaagcctttg ggaccaagga aacttcccc tgatcatcaa gaatcttaag 300
43 atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360
44 ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca ggcctgacc 420
45 ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480
46 aaaacatac agggggggaa gacctctcc gtgtctcagc tggagctcca ggatagtggc 540
47 acctggacat gactgtctt gcagaaccag aagaagggtg agttcaaaat agacatcgtg 600
48 gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acaggtggag 660
49 ttctccttcc cactgcctt tacagttgaa aagctgacgg gcagtggcga gctgtggtg 720
50 caggcggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780
51 gtgtctgtaa aacgggttac ccaggacct aagctccaga tgggcaagaa gctcccgtc 840
52 cacctcacc cgtccccagg cttgcctcag tatgtgtggt ctggaaacct caccctggcc 900
53 cttgaagcga aaacaggaaa gttgcatcag gaagtgaacc tgggtggtgat gagagccact 960
54 cagctccaga aaaatttgac ctgtgaggtg tggggaccca cctcccctaa gctgatgctg 1020
55 agcttgaaac tggagaacaa ggaggcaag gtctcgaagc gggagaagcc ggtgtgggtg 1080
56 ctgaaccctg aggcggggat gtggcagtg gtctgagtg actcgggaca ggtcctgctg 1140
57 gaatccaaca tcaaggttct gccacatgg tccaccccg tgacgcgga tcccaaactc 1200

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58 tgctacttgc tagatggaat cctcttcacg tacggagtca tcatcacagc cctgtacctg 1260
59 agagcaaaat tcagcaggag tgcagagact gctgccaacc tgcaggaccc caaccagctc 1320
60 tacaatgagc tcaatctagg gcgaagagag gaatatgacg tcttgagaga gaagcgggct 1380
61 cgggatccag agatgggagg caaacagcag aggaggagga acccccagga aggcgtatac 1440
62 aatgcactgc agaaagacaa gatgccagaa gcctacagtg agatcggcac aaaaggcgag 1500
63 aggcggagag gcaaggggca cgatggcctt taccaggaca gccacttcca agcagtgcag 1560
64 ttcgggaaca gaagagagag agaagggtca gaactcaca ggacccttgg gttaagagcc 1620
65 cgccccaaag gtgaaagcac ccagcagagt agccaatcct gtgccagcgt cttcagcatc 1680
66 cccactctgt ggagtccatg gccaccacgt agcagctccc agctctaa 1728

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68 <210> SEQ ID NO: 2

69 <211> LENGTH: 1389

70 <212> TYPE: DNA

71 <213> ORGANISM: Homo sapiens

73 <400> SEQUENCE: 2

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75 gcagccactc agggaaacaa agtggtgctg ggcaaaaaag gggatacagt ggaactgacc 120
76 tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180
77 attctgggaa atcagggtc cttcttaact aaagggtccat ccaagctgaa tgatcgcgct 240
78 gactcaagaa gaagcctttg ggaccaagga aacttcccc tgatcatcaa gaatcttaag 300
79 atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360
80 ctagtgttcg gattgactgc caactctgac acccacctgc ttcaggggca ggcctgacc 420
81 ctgaccttgg agagcccccc tggtagtagc ccctcagtgc aatgtaggag tccaaggggt 480
82 aaaaacatac aggggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540
83 acctggacat gcactgtctt gcagaaccag aagaagggtg agttcaaaat agacatcgtg 600
84 gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acagggtggg 660
85 ttctccttcc cactgcctt tacagttgaa aagctgacgg gcagtggcga gctgtggtgg 720
86 caggcggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780
87 gtgtctgtaa aacgggttac ccaggaccct aagctccaga tgggcaagaa gctcccgtc 840
88 cacctacccc tgccccaggc cttgcctcag tatgctggct ctggaaacct caccctggcc 900
89 cttgaagcga aaacaggaaa gtgtcatcag gaagtgaacc tgggtggtgat gagagccact 960
90 cagctccaga aaaatttgac ctgtgaggtg tggggaccca cctcccctaa gctgatgctg 1020
91 agcttgaaac tggagaacaa ggaggcaaa gtctcgaagc gggagaagcc ggtgtgggtg 1080
92 ctgaaccctg aggcggggat gtggcagtg ctgctgagtg actcgggaca ggtcctgctg 1140
93 gaatccaaca tcaaggttct gccacatgg tccaccccg tgacgcgga tccgcagctc 1200
94 tgctatatcc tggatgccat cctgtttttg tatggtattg tccttaccct gctctactgt 1260
95 cgactcaaga tccaggtccg aaaggcagac atagccagcc gtgagaaatc agatgctgtc 1320
96 tacacgggcc tgaacacccg gaaccaggag acatatgaga ctctgaaaca tgagaaacca 1380
97 cccaatag 1389

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99 <210> SEQ ID NO: 3

100 <211> LENGTH: 1599

101 <212> TYPE: DNA

102 <213> ORGANISM: Homo sapiens

104 <400> SEQUENCE: 3

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105 atgaaccggg gagtcccttt taggcacttg cttctggtgc tgcaactggc gctcctccca 60
106 gcagccactc agggaaacaa agtggtgctg ggcaaaaaag gggatacagt ggaactgacc 120
107 tgtacagctt cccagaagaa gagcatacaa ttccactgga aaaactccaa ccagataaag 180
108 attctgggaa atcagggtc cttcttaact aaagggtccat ccaagctgaa tgatcgcgct 240
109 gactcaagaa gaagcctttg ggaccaagga aacttcccc tgatcatcaa gaatcttaag 300
110 atagaagact cagatactta catctgtgaa gtggaggacc agaaggagga ggtgcaattg 360

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111 ctagtggttcg gattgactgc caactctgac acccacctgc ttcaggggca gaggctgacc 420
112 ctgaccttgg agagcccccc tggtagtagc cctcagtgac aatgtaggag tccaaggggt 480
113 aaaaacatac aggggggggaa gaccctctcc gtgtctcagc tggagctcca ggatagtggc 540
114 acctggacat gcaactgtctt gcagaaccag aagaaggtgg agttcaaaat agacatcgtg 600
115 gtgctagctt tccagaaggc ctccagcata gtctataaga aagaggggga acaggtggag 660
116 ttctccttcc cactcgcctt tacagttgaa aagctgacgg gcagtgggcga gctgtggtgg 720
117 caggcgaggaga gggcttcctc ctccaagtct tggatcacct ttgacctgaa gaacaaggaa 780
118 gtgtctgtaa aacgggttac ccaggaccct aagctccaga tgggcaagaa gctcccgtc 840
119 cacctacccc tgccccaggc cttgcctcag tatgtggtct ctggaaacct caccctggcc 900
120 cttgaagcga aaacaggaaa gttgcatcag gaagtgaacc tgggtggtgat gagagccact 960
121 cagctccaga aaaatttgac ctgtgaggtg tggggaccca cctcccctaa gctgatgctg 1020
122 agcttgaaac tggagaacaa ggaggcaaag gtctcgaagc gggagaagcc ggtgtgggtg 1080
123 ctgaaccctg aggcggggat gtggcagtg ctgctgagtg actcgggaca ggtcctgctg 1140
124 gaatccaaca tcaaggttct gccacatgg tccaccccg tgcacgcgga tcccaaactc 1200
125 tgctacctgc tggatggaat cctcttcac tatggtgtca ttctcactgc cttgttcctg 1260
126 agagtgaagt tcagcaggag cgcagagccc cccgcgtacc agcagggcca gaaccagctc 1320
127 tataacgagc tcaatctagg acgaagagag gactacgatg ttttggacaa gagacgtggc 1380
128 cgggacctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 1440
129 gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 1500
130 cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 1560
131 tacgacgccc ttcacatgca ggccctgccc cctcgctaa 1599

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133 <210> SEQ ID NO: 4

134 <211> LENGTH: 575

135 <212> TYPE: PRT

136 <213> ORGANISM: Homo sapiens

138 <400> SEQUENCE: 4

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139 Met Asn Arg Gly Val Pro Phe Arg His Leu Leu Leu Val Leu Gln Leu
140 1 5 10 15
141 Ala Leu Leu Pro Ala Ala Thr Gln Gly Asn Lys Val Val Leu Gly Lys
142 20 25 30
143 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
144 35 40 45
145 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
146 50 55 60
147 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
148 65 70 75 80
149 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
150 85 90 95
151 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
152 100 105 110
153 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
154 115 120 125
155 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
156 130 135 140
157 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
158 145 150 155 160
159 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
160 165 170 175
161 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys

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162          180          185          190
163 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
164          195          200          205
165 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
166          210          215          220
167 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
168 225          230          235          240
169 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
170          245          250          255
171 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
172          260          265          270
173 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
174          275          280          285
175 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
176          290          295          300
177 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
178 305          310          315          320
179 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
180          325          330          335
181 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
182          340          345          350
183 Lys Arg Glu Lys Pro Val Trp Val Leu Asn Pro Glu Ala Gly Met Trp
184          355          360          365
185 Gln Cys Leu Leu Ser Asp Ser Gly Gln Val Leu Leu Glu Ser Asn Ile
186          370          375          380
187 Lys Val Leu Pro Thr Trp Ser Thr Pro Val His Ala Asp Pro Lys Leu
188 385          390          395          400
189 Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Ile Thr
190          405          410          415
191 Ala Leu Tyr Leu Arg Ala Lys Phe Ser Arg Ser Ala Glu Thr Ala Ala
192          420          425          430
193 Asn Leu Gln Asp Pro Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
194          435          440          445
195 Arg Glu Glu Tyr Asp Val Leu Glu Lys Lys Arg Ala Arg Asp Pro Glu
196          450          455          460
197 Met Gly Gly Lys Gln Gln Arg Arg Arg Asn Pro Gln Glu Gly Val Tyr
198 465          470          475          480
199 Asn Ala Leu Gln Lys Asp Lys Met Pro Glu Ala Tyr Ser Glu Ile Gly
200          485          490          495
201 Thr Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
202          500          505          510
203 Asp Ser His Phe Gln Ala Val Gln Phe Gly Asn Arg Arg Glu Arg Glu
204          515          520          525
205 Gly Ser Glu Leu Thr Arg Thr Leu Gly Leu Arg Ala Arg Pro Lys Gly
206          530          535          540
207 Glu Ser Thr Gln Gln Ser Ser Gln Ser Cys Ala Ser Val Phe Ser Ile
208 545          550          555          560
209 Pro Thr Leu Trp Ser Pro Trp Pro Pro Ser Ser Ser Ser Gln Leu
210          565          570          575

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213 <210> SEQ ID NO: 5
214 <211> LENGTH: 462
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 5
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220 1 5 10 15
221 Ala Leu Leu Pro Ala Ala Thr Gln Gly Asn Lys Val Val Leu Gly Lys
222 20 25 30
223 Lys Gly Asp Thr Val Glu Leu Thr Cys Thr Ala Ser Gln Lys Lys Ser
224 35 40 45
225 Ile Gln Phe His Trp Lys Asn Ser Asn Gln Ile Lys Ile Leu Gly Asn
226 50 55 60
227 Gln Gly Ser Phe Leu Thr Lys Gly Pro Ser Lys Leu Asn Asp Arg Ala
228 65 70 75 80
229 Asp Ser Arg Arg Ser Leu Trp Asp Gln Gly Asn Phe Pro Leu Ile Ile
230 85 90 95
231 Lys Asn Leu Lys Ile Glu Asp Ser Asp Thr Tyr Ile Cys Glu Val Glu
232 100 105 110
233 Asp Gln Lys Glu Glu Val Gln Leu Leu Val Phe Gly Leu Thr Ala Asn
234 115 120 125
235 Ser Asp Thr His Leu Leu Gln Gly Gln Ser Leu Thr Leu Thr Leu Glu
236 130 135 140
237 Ser Pro Pro Gly Ser Ser Pro Ser Val Gln Cys Arg Ser Pro Arg Gly
238 145 150 155 160
239 Lys Asn Ile Gln Gly Gly Lys Thr Leu Ser Val Ser Gln Leu Glu Leu
240 165 170 175
241 Gln Asp Ser Gly Thr Trp Thr Cys Thr Val Leu Gln Asn Gln Lys Lys
242 180 185 190
243 Val Glu Phe Lys Ile Asp Ile Val Val Leu Ala Phe Gln Lys Ala Ser
244 195 200 205
245 Ser Ile Val Tyr Lys Lys Glu Gly Glu Gln Val Glu Phe Ser Phe Pro
246 210 215 220
247 Leu Ala Phe Thr Val Glu Lys Leu Thr Gly Ser Gly Glu Leu Trp Trp
248 225 230 235 240
249 Gln Ala Glu Arg Ala Ser Ser Ser Lys Ser Trp Ile Thr Phe Asp Leu
250 245 250 255
251 Lys Asn Lys Glu Val Ser Val Lys Arg Val Thr Gln Asp Pro Lys Leu
252 260 265 270
253 Gln Met Gly Lys Lys Leu Pro Leu His Leu Thr Leu Pro Gln Ala Leu
254 275 280 285
255 Pro Gln Tyr Ala Gly Ser Gly Asn Leu Thr Leu Ala Leu Glu Ala Lys
256 290 295 300
257 Thr Gly Lys Leu His Gln Glu Val Asn Leu Val Val Met Arg Ala Thr
258 305 310 315 320
259 Gln Leu Gln Lys Asn Leu Thr Cys Glu Val Trp Gly Pro Thr Ser Pro
260 325 330 335
261 Lys Leu Met Leu Ser Leu Lys Leu Glu Asn Lys Glu Ala Lys Val Ser
262 340 345 350

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VERIFICATION SUMMARY

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